

SEQUENCE LISTING

<110> BIOMERIEUX
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

<120> Composition comprising the polyprotein NS3/NS4 and the polypeptide NS5b of HCV, expression vectors including the corresponding nucleic sequences and their therapeutic use

<130> ADENOVIR

<160> 27

<170> PatentIn version 3.1

<210> 1
<211> 2844
<212> DNA
<213> Artificial sequence

<220>
<223> sequence coding for NS3NS4

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<221> CDS
<222> (1)..(2844)
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Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Asp Gly	
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Glu Val Gln Val Leu Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys	
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Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr	
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ctg gcc ggc ccg aag ggt cca atc acc caa atg tac acc aat gta gac	240
Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp	
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Gln Asp Leu Val Gly Trp Pro Ala Pro Pro Gly Ala Arg Ser Met Thr	
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ccg tgc acc tgc ggc agc tcg gac ctt tac ttg gtc acg agg cat gcc	336
Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala	
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Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu	
115 120 125	

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acc cgg ggg gtt gcg aag gcg gtg gac ttc ata ccc gtt gag tct atg Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Ser Met 165 170 175	528
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gcc gta ccg caa aca ttc caa gtg gca cat tta cac gct ccc act ggc Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly 195 200 205	624
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aaa gcc atc ccc att gag gcc atc aag ggg gga agg cat ctc atc ttc Lys Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Ile Phe 355 360 365	1104

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gcc cac ttc ctg tcc caa acc aag cag gca gga gac aac ttc ccc tac Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr 545 550 555 560	1680
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ccc tcc gcc gag gac ctg gtt aac ttg ctc cct gcc atc ctc tcc ccc 2592
 Pro Ser Ala Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro
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 Gly Ala Leu Val Val Gly Ile Val Cys Ala Ala Ile Leu Arg Arg His
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 Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala
 885 890 895

ttc gct tcg cgg ggt aac cac gtt tcc ccc acg cac tac gtg cct gag 2736
 Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val Pro Glu
 900 905 910

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 Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile
 915 920 925

act cag ctg ctg aag agg ctt cac cag tgg att aat gag gac tgc tcc 2832
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acg cca tgc taa 2844
 Thr Pro Cys
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<220>
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Glu Val Gln Val Leu Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
 35 40 45

Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
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Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
 65 70 75 80

Gln Asp Leu Val Gly Trp Pro Ala Pro Gly Ala Arg Ser Met Thr
 85 90 95

Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
 100 105 110

Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	115	120	125
Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	130	135	140
Leu	Cys	Pro	Ser	Gly	His	Val	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	145	150	155
Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Ile	Pro	Val	Glu	Ser	Met	165	170	175
Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	180	185	190
Ala	Val	Pro	Gln	Thr	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	195	200	205
Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	210	215	220
Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	225	230	235
Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Glu	Pro	Asn	Ile	Arg	Thr	Gly	245	250	255
Val	Arg	Thr	Ile	Thr	Thr	Gly	Gly	Pro	Ile	Thr	Tyr	Ser	Thr	Tyr	Gly	260	265	270
Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	275	280	285
Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Trp	Thr	Thr	Ile	Leu	Gly	Ile	290	295	300
Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	305	310	315
Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Ile	Thr	Val	Pro	His	Pro	Asn	325	330	335
Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	340	345	350
Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile	Phe	355	360	365
Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Thr	Gly	370	375	380
Leu	Gly	Leu	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	385	390	395
Ile	Pro	Thr	Ser	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	405	410	415
Thr	Gly	Phe	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	420	425	430

Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	435	440	445
Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	450	455	460
Arg	Thr	Gly	Arg	Gly	Arg	Ser	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	465	470	475
Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	485	490	495
Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Thr	Val	500	505	510
Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	515	520	525
His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	530	535	540
Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	545	550	555
Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	565	570	575
Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	580	585	590
Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	595	600	605
Glu	Ile	Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Phe	Val	Met	Ala	Cys	Met	610	615	620
Ser	Ala	Asp	Leu	Glu	Val	Val	Thr	Ser	Thr	Trp	Val	Leu	Val	Gly	Gly	625	630	635
Val	Leu	Ala	Ala	Leu	Ala	Ala	Tyr	Cys	Leu	Thr	Thr	Gly	Ser	Val	Val	645	650	655
Ile	Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Arg	Pro	Ala	Val	Val	Pro	Asp	660	665	670
Arg	Glu	Val	Leu	Tyr	Arg	Glu	Phe	Asp	Glu	Met	Glu	Glu	Cys	Ala	Ser	675	680	685
His	Leu	Pro	Tyr	Ile	Glu	Gln	Gly	Met	Gln	Leu	Ala	Glu	Gln	Phe	Lys	690	695	700
Gln	Gln	Ala	Leu	Gly	Leu	Leu	Gln	Thr	Ala	Thr	Lys	Gln	Ala	Glu	Ala	705	710	715
Ala	Ala	Pro	Val	Val	Glu	Ser	Arg	Trp	Arg	Ala	Leu	Glu	Ala	Phe	Trp	725	730	735
Ala	Lys	His	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln	Tyr	Leu	Ala	Gly	740	745	750

Leu Ser Thr Leu Pro Gly Asn Pro Ala Ile Ala Ser Leu Met Ala Phe
 755 760 765
 Thr Ala Ser Ile Thr Ser Pro Leu Thr Thr Gln Asn Thr Leu Leu Phe
 770 775 780
 Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Leu Ala Pro Pro Ser Ala
 785 790 795 800
 Ala Ser Ala Phe Val Gly Ala Gly Ile Ala Gly Ala Ala Ile Gly Ser
 805 810 815
 Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala
 820 825 830
 Gly Val Ala Gly Ala Leu Val Ala Phe Lys Val Met Ser Gly Glu Ala
 835 840 845
 Pro Ser Ala Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro
 850 855 860
 Gly Ala Leu Val Val Gly Ile Val Cys Ala Ala Ile Leu Arg Arg His
 865 870 875 880
 Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala
 885 890 895
 Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val Pro Glu
 900 905 910
 Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile
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 Thr Pro Cys
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gcg gag gag agc aag ttg ccc atc aat ccg ttg agc aac tct ttg ctg
 Ala Glu Glu Ser Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Leu
 20 25 30

96

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cgg	cag	aag	aag	gtc	acc	ttt	gac	aga	ctg	caa	gtc	ctg	gac	gac	cac	192
Arg	Gln	Lys	Lys	Val	Thr	Phe	Asp	Arg	Leu	Gln	Val	Leu	Asp	Asp	His	
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tac	cgg	gac	gtg	ctc	aag	gag	atg	aag	gcg	aag	gcg	tcc	aca	gtt	aag	240
Tyr	Arg	Asp	Val	Leu	Lys	Glu	Met	Lys	Ala	Lys	Ala	Ser	Thr	Val	Lys	
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tcg	gcc	aaa	tcc	aaa	ttt	ggc	tac	ggg	gcg	aag	gac	gtc	cgg	agc	cta	336
Ser	Ala	Lys	Ser	Lys	Phe	Gly	Tyr	Gly	Ala	Lys	Asp	Val	Arg	Ser	Leu	
			100					105					110			
tcc	agc	agg	gcc	gtc	aac	cac	atc	cgc	tcc	gtg	tgg	gag	gac	ttg	ctg	384
Ser	Ser	Arg	Ala	Val	Asn	His	Ile	Arg	Ser	Val	Trp	Glu	Asp	Leu	Leu	
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gaa	gac	act	gaa	aca	cca	att	gat	acc	acc	atc	atg	gca	aaa	aat	gag	432
Glu	Asp	Thr	Glu	Thr	Pro	Ile	Asp	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu	
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gtt	ttc	tgc	gtc	caa	cca	gag	aaa	gga	ggc	cgc	aag	cca	gct	cgc	ctt	480
Val	Phe	Cys	Val	Gln	Pro	Glu	Lys	Gly	Gly	Arg	Lys	Pro	Ala	Arg	Leu	
145					150					155					160	
atc	gta	ttc	cca	gac	ctg	ggg	gta	cgt	gta	tgc	gag	aag	atg	gcc	ctt	528
Ile	Val	Phe	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	
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tac	gac	gtg	gtc	tcc	acc	ctt	cct	cag	gcc	gtg	atg	ggc	ccc	tca	tac	576
Tyr	Asp	Val	Val	Ser	Thr	Leu	Pro	Gln	Ala	Val	Met	Gly	Pro	Ser	Tyr	
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gga	ttc	cag	tac	tct	cct	ggg	cag	cgg	gtc	gag	ttc	ctg	gtg	aat	acc	624
Gly	Phe	Gln	Tyr	Ser	Pro	Gly	Gln	Arg	Val	Glu	Phe	Leu	Val	Asn	Thr	
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Trp	Lys	Ser	Lys	Lys	Cys	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys	
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Phe	Asp	Ser	Thr	Val	Thr	Glu	Asn	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	
225					230					235					240	
tac	caa	tgt	tgt	gac	ttg	gcc	ccc	gaa	gcc	aga	cag	gcc	ata	aag	tcg	768
Tyr	Gln	Cys	Cys	Asp	Leu	Ala	Pro	Glu	Ala	Arg	Gln	Ala	Ile	Lys	Ser	
				245					250					255		
ctc	aca	gag	cgg	ctc	tac	atc	ggg	ggt	ccc	ctg	act	aat	tca	aaa	ggg	816
Leu	Thr	Glu	Arg	Leu	Tyr	Ile	Gly	Gly	Pro	Leu	Thr	Asn	Ser	Lys	Gly	
			260					265					270			

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agc tgc ggc aat acc ctc aca tgc tac ttg aaa gcc act gcg gcc tgt Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Cys 290 295 300	912
cga gct gca aag ctc cag gac tgc acg atg ctc gtg aac gga gac gac Arg Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp 305 310 315 320	960
ctt gtc gtt atc tgc gaa agc gcg gga acc cag gag gat gcg gcg agc Leu Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser 325 330 335	1008
cta cga gtc ttc acg gag gct atg act agg tac tct gcc ccc ccc ggg Leu Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly 340 345 350	1056
gac ccg ccc caa cca gaa tac gac ttg gag ctg ata acg tca tgc tcc Asp Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser 355 360 365	1104
tcc aat gtg tcg gtc gcg cac gat gca tcc ggc aaa agg gtg tac tac Ser Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr 370 375 380	1152
ctc acc cgt gac ccc acc acc ccc ctc gca cgg gct gcg tgg gag aca Leu Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr 385 390 395 400	1200
gtt aga cac act cca gtc aac tcc tgg cta ggc aat atc atc atg tat Val Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr 405 410 415	1248
gcg ccc acc cta tgg gcg agg atg att ctg atg act cat ttc ttc tct Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser 420 425 430	1296
atc ctt cta gct cag gag caa ctt gaa aaa gcc ctg gat tgt cag atc Ile Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile 435 440 445	1344
tac ggg gcc tgc tac tcc att gag cca ctt gac cta cct cag atc atc Tyr Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile 450 455 460	1392
gaa cga ctc cat ggt ctt agc gca ttt tca ctc cat agt tac tct cca Glu Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro 465 470 475 480	1440
ggt gag atc aat agg gtg gct tca tgc ctc agg aaa ctt ggg gta cca Gly Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro 485 490 495	1488
ccc ttg cga gtc tgg aga cat cgg gcc aga agt gtc cgc gct aag ttg Pro Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Lys Leu 500 505 510	1536

[illegible]

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<210> 4
<211> 592
<212> PRT
<213> Artificial sequence
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<220>
<223> sequence coding for NS5b
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<400> 4

Met 1	Ser	Met	Ser	Tyr 5	Thr	Trp	Thr	Gly	Ala 10	Leu	Ile	Thr	Pro	Cys 15	Ala
Ala	Glu	Glu	Ser 20	Lys	Leu	Pro	Ile	Asn 25	Pro	Leu	Ser	Asn	Ser 30	Leu	Leu
Arg	His	His 35	Ser	Met	Val	Tyr	Ser 40	Thr	Thr	Ser	Arg	Ser 45	Ala	Ser	Leu
Arg	Gln 50	Lys	Lys	Val	Thr	Phe 55	Asp	Arg	Leu	Gln	Val 60	Leu	Asp	Asp	His
Tyr 65	Arg	Asp	Val	Leu	Lys 70	Glu	Met	Lys	Ala	Lys 75	Ala	Ser	Thr	Val	Lys 80
Ala	Arg	Leu	Leu 85	Ser	Ile	Glu	Glu	Ala	Cys 90	Lys	Leu	Thr	Pro	Pro 95	His
Ser	Ala	Lys	Ser 100	Lys	Phe	Gly	Tyr	Gly 105	Ala	Lys	Asp	Val	Arg	Ser	Leu
Ser	Ser	Arg 115	Ala	Val	Asn	His	Ile 120	Arg	Ser	Val	Trp	Glu 125	Asp	Leu	Leu
Glu	Asp 130	Thr	Glu	Thr	Pro	Ile 135	Asp	Thr	Thr	Ile	Met 140	Ala	Lys	Asn	Glu

Val	Phe	Cys	Val	Gln	Pro	Glu	Lys	Gly	Gly	Arg	Lys	Pro	Ala	Arg	Leu	145	150	155	160
Ile	Val	Phe	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	165	170	175	
Tyr	Asp	Val	Val	Ser	Thr	Leu	Pro	Gln	Ala	Val	Met	Gly	Pro	Ser	Tyr	180	185	190	
Gly	Phe	Gln	Tyr	Ser	Pro	Gly	Gln	Arg	Val	Glu	Phe	Leu	Val	Asn	Thr	195	200	205	
Trp	Lys	Ser	Lys	Lys	Cys	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys	210	215	220	
Phe	Asp	Ser	Thr	Val	Thr	Glu	Asn	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	225	230	235	240
Tyr	Gln	Cys	Cys	Asp	Leu	Ala	Pro	Glu	Ala	Arg	Gln	Ala	Ile	Lys	Ser	245	250	255	
Leu	Thr	Glu	Arg	Leu	Tyr	Ile	Gly	Gly	Pro	Leu	Thr	Asn	Ser	Lys	Gly	260	265	270	
Gln	Asn	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	275	280	285	
Ser	Cys	Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Thr	Ala	Ala	Cys	290	295	300	
Arg	Ala	Ala	Lys	Leu	Gln	Asp	Cys	Thr	Met	Leu	Val	Asn	Gly	Asp	Asp	305	310	315	320
Leu	Val	Val	Ile	Cys	Glu	Ser	Ala	Gly	Thr	Gln	Glu	Asp	Ala	Ala	Ser	325	330	335	
Leu	Arg	Val	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly	340	345	350	
Asp	Pro	Pro	Gln	Pro	Glu	Tyr	Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser	355	360	365	
Ser	Asn	Val	Ser	Val	Ala	His	Asp	Ala	Ser	Gly	Lys	Arg	Val	Tyr	Tyr	370	375	380	
Leu	Thr	Arg	Asp	Pro	Thr	Thr	Pro	Leu	Ala	Arg	Ala	Ala	Trp	Glu	Thr	385	390	395	400
Val	Arg	His	Thr	Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Met	Tyr	405	410	415	
Ala	Pro	Thr	Leu	Trp	Ala	Arg	Met	Ile	Leu	Met	Thr	His	Phe	Phe	Ser	420	425	430	
Ile	Leu	Leu	Ala	Gln	Glu	Gln	Leu	Glu	Lys	Ala	Leu	Asp	Cys	Gln	Ile	435	440	445	
Tyr	Gly	Ala	Cys	Tyr	Ser	Ile	Glu	Pro	Leu	Asp	Leu	Pro	Gln	Ile	Ile	450	455	460	

Glu Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro
 465 470 475 480
 Gly Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro
 485 490 495
 Pro Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Lys Leu
 500 505 510
 Leu Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn
 515 520 525
 Trp Ala Val Arg Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser
 530 535 540
 Gln Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Asn Gly Gly Asp
 545 550 555 560
 Ile Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Trp Phe Met Leu Cys
 565 570 575
 Leu Leu Leu Leu Ser Val Gly Val Gly Ile Tyr Leu Leu Pro Asn Arg
 580 585 590

<210> 5
 <211> 1344
 <212> DNA
 <213> Artificial sequence

<220>
 <223> sequence coding for NS5a

<220>
 <221> CDS
 <222> (1)..(1344)
 <223>

<400> 5
 atg tcc ggc tcg tgg cta agg gat gtt tgg gac tgg ata tgc acg gtg 48
 Met Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys Thr Val
 1 5 10 15
 ttg act gac ttc aag acc tgg ctc cag tcc aag ctc ctg ccg aaa ttg 96
 Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro Lys Leu
 20 25 30
 ccg gga gtc cct ttc ttc tca tgc caa cgc ggg tac aag gga gtc tgg 144
 Pro Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp
 35 40 45
 cgg ggg gac ggc atc atg caa acc acc tgc cca tgt gga gca caa att 192
 Arg Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile
 50 55 60
 acc gga cat gtc aaa aac ggt tcc atg agg atc gtt ggg cct aaa acc 240
 Thr Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro Lys Thr
 65 70 75 80

tgc agc aac acg tgg cac gga acg ttc ccc atc aac gcg tac acc aca	288
Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr	
85 90 95	
ggc ccc tgc aca ccc tcc ccg gcg ccg aac tat tcc agg gcg ctg tgg	336
Gly Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala Leu Trp	
100 105 110	
cgg gtg gct gct gaa gag tac gtg gag att acg cgg gtg ggg gac ttc	384
Arg Val Ala Ala Glu Glu Tyr Val Glu Ile Thr Arg Val Gly Asp Phe	
115 120 125	
cac tac gtg acg ggt atg acc acc gac aac gta aaa tgc ccg tgc cag	432
His Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro Cys Gln	
130 135 140	
gtc ccg gcc ccc gaa ttc ttc act gaa ttg gac ggg gtg ccg ttg cac	480
Val Pro Ala Pro Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His	
145 150 155 160	
agg tac gct ccg gcg tgc aga cct ctc cta ccg gtg gat gtc aca ttc	528
Arg Tyr Ala Pro Ala Cys Arg Pro Leu Leu Arg Val Asp Val Thr Phe	
165 170 175	
cag gtc ggg ctc aac caa tac ctg gtt ggg tca cag ctc cca tgc gag	576
Gln Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro Cys Glu	
180 185 190	
cct gag ccg gat gtg gca gtg ctc act tcc atg ctc acc gac ccc tcc	624
Pro Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp Pro Ser	
195 200 205	
cac att aca gca gag acg gct aaa cgt agg ccg gcc agg ggg tct ccc	672
His Ile Thr Ala Glu Thr Ala Lys Arg Arg Pro Ala Arg Gly Ser Pro	
210 215 220	
ccc tcc ttg gcc agc tct tca gct agc caa ttg tct gcg cct tcc ttg	720
Pro Ser Leu Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu	
225 230 235 240	
aag gca aca tgc act acc cac cat gac tcc ccg gac gct gac ctc atc	768
Lys Ala Thr Cys Thr Thr His His Asp Ser Pro Asp Ala Asp Leu Ile	
245 250 255	
gag gcc aac ctc ctg tgg ccg cag gag atg ggc gga aac atc acc cgt	816
Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg	
260 265 270	
gtg gag tca gag aat aag gtg gta att ttg gac tct ttc gac ccg ctt	864
Val Glu Ser Glu Asn Lys Val Val Ile Leu Asp Ser Phe Asp Pro Leu	
275 280 285	
cga gcg gaa gag gat gag agg gaa gta tcc gtt gca gca gag atc ctg	912
Arg Ala Glu Glu Asp Glu Arg Glu Val Ser Val Ala Ala Glu Ile Leu	
290 295 300	
cga aaa tcc aag aag ttc ccc ccc gcg ttg ccc ata tgg gca cgc ccg	960
Arg Lys Ser Lys Lys Phe Pro Pro Ala Leu Pro Ile Trp Ala Arg Pro	
305 310 315 320	

gat tac aac cct cca ctg tta gag tcc tgg aaa agt ccg gac tac gtc 1008
 Asp Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Ser Pro Asp Tyr Val
 325 330 335

cct ccg gcg gtg cat ggg tgc cca ttg ccg cct acc acg ggc cct cca 1056
 Pro Pro Ala Val His Gly Cys Pro Leu Pro Pro Thr Thr Gly Pro Pro
 340 345 350

ata ccg cct cca cgg aaa aag agg acg gtt gtt ctg aca gag tcc acc 1104
 Ile Pro Pro Pro Arg Lys Lys Arg Thr Val Val Leu Thr Glu Ser Thr
 355 360 365

gtg tct tct gcc ttg gcg gag ctg gct act aag act ttc ggc agc tcc 1152
 Val Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly Ser Ser
 370 375 380

gga tcg tcg gcc gtt gac agc ggc acg gcg acc gcc cct ccc gat cag 1200
 Gly Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Pro Pro Asp Gln
 385 390 395 400

acc tct gac gac ggt gac aaa gaa tct gac att gag tcg tac tcc tcc 1248
 Thr Ser Asp Asp Gly Asp Lys Glu Ser Asp Ile Glu Ser Tyr Ser Ser
 405 410 415

atg ccc ccc ctt gag ggg gag ccg ggg gac cct gat ctc agc gac ggg 1296
 Met Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly
 420 425 430

tct tgg tct acc gtg agc ggg gag gcc ggc gac gac atc gtc tgc tgc 1344
 Ser Trp Ser Thr Val Ser Gly Glu Ala Gly Asp Asp Ile Val Cys Cys
 435 440 445

<210> 6
 <211> 448
 <212> PRT
 <213> Artificial sequence

<220>
 <223> sequence coding for NS5a

<400> 6

Met Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys Thr Val
 1 5 10 15

Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro Lys Leu
 20 25 30

Pro Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp
 35 40 45

Arg Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile
 50 55 60

Thr Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro Lys Thr
 65 70 75 80

Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr Thr Thr
 85 90 95

Gly	Pro	Cys	Thr	Pro	Ser	Pro	Ala	Pro	Asn	Tyr	Ser	Arg	Ala	Leu	Trp	100	105	110
Arg	Val	Ala	Ala	Glu	Glu	Tyr	Val	Glu	Ile	Thr	Arg	Val	Gly	Asp	Phe	115	120	125
His	Tyr	Val	Thr	Gly	Met	Thr	Thr	Asp	Asn	Val	Lys	Cys	Pro	Cys	Gln	130	135	140
Val	Pro	Ala	Pro	Glu	Phe	Phe	Thr	Glu	Leu	Asp	Gly	Val	Arg	Leu	His	145	150	155
Arg	Tyr	Ala	Pro	Ala	Cys	Arg	Pro	Leu	Leu	Arg	Val	Asp	Val	Thr	Phe	165	170	175
Gln	Val	Gly	Leu	Asn	Gln	Tyr	Leu	Val	Gly	Ser	Gln	Leu	Pro	Cys	Glu	180	185	190
Pro	Glu	Pro	Asp	Val	Ala	Val	Leu	Thr	Ser	Met	Leu	Thr	Asp	Pro	Ser	195	200	205
His	Ile	Thr	Ala	Glu	Thr	Ala	Lys	Arg	Arg	Pro	Ala	Arg	Gly	Ser	Pro	210	215	220
Pro	Ser	Leu	Ala	Ser	Ser	Ser	Ala	Ser	Gln	Leu	Ser	Ala	Pro	Ser	Leu	225	230	235
Lys	Ala	Thr	Cys	Thr	Thr	His	His	Asp	Ser	Pro	Asp	Ala	Asp	Leu	Ile	245	250	255
Glu	Ala	Asn	Leu	Leu	Trp	Arg	Gln	Glu	Met	Gly	Gly	Asn	Ile	Thr	Arg	260	265	270
Val	Glu	Ser	Glu	Asn	Lys	Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	275	280	285
Arg	Ala	Glu	Glu	Asp	Glu	Arg	Glu	Val	Ser	Val	Ala	Ala	Glu	Ile	Leu	290	295	300
Arg	Lys	Ser	Lys	Lys	Phe	Pro	Pro	Ala	Leu	Pro	Ile	Trp	Ala	Arg	Pro	305	310	315
Asp	Tyr	Asn	Pro	Pro	Leu	Leu	Glu	Ser	Trp	Lys	Ser	Pro	Asp	Tyr	Val	325	330	335
Pro	Pro	Ala	Val	His	Gly	Cys	Pro	Leu	Pro	Pro	Thr	Thr	Gly	Pro	Pro	340	345	350
Ile	Pro	Pro	Pro	Arg	Lys	Lys	Arg	Thr	Val	Val	Leu	Thr	Glu	Ser	Thr	355	360	365
Val	Ser	Ser	Ala	Leu	Ala	Glu	Leu	Ala	Thr	Lys	Thr	Phe	Gly	Ser	Ser	370	375	380
Gly	Ser	Ser	Ala	Val	Asp	Ser	Gly	Thr	Ala	Thr	Ala	Pro	Pro	Asp	Gln	385	390	395
Thr	Ser	Asp	Asp	Gly	Asp	Lys	Glu	Ser	Asp	Ile	Glu	Ser	Tyr	Ser	Ser	405	410	415

Met Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly
 420 425 430

Ser Trp Ser Thr Val Ser Gly Glu Ala Gly Asp Asp Ile Val Cys Cys
 435 440 445

<210> 7
 <211> 2241
 <212> DNA
 <213> Artificial sequence

<220>
 <223> sequence coding for CE1E2

<220>
 <221> CDS
 <222> (1)..(2241)
 <223>

<400> 7

atg agc aca aat cct aaa cct caa aga aaa acc aaa cgt aac acc aac	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
cgc cgc cca cag gac gtt aag ttc ccg ggc ggt ggt cag atc gtt ggt	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
gga gtt tac ctg ttg ccg cgc agg ggc ccc agg ttg ggt gtg cgc gcg	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
act agg aag act tcc gag cgg tcg caa cct cgt gga agg cga caa cct	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
atc ccc aag gct cgc cgg ccc gag ggt agg acc tgg gct cag ccc ggg	240
Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly	
65 70 75 80	
tac cct tgg ccc ctc tat ggc aac gag ggt atg ggg tgg gca gga tgg	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp	
85 90 95	
ctc ctg tca ccc cgt ggc tct cgg cct agt tgg ggc ccc aca gac ccc	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
cgg cgt agg tcg cgt aat ttg ggt aag gtc atc gat acc ctt aca tgc	384
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
ggc ttc gcc gac ctc atg ggg tac att ccg ctt gtc ggc gcc ccc cta	432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu	
130 135 140	
gga ggc gct gcc agg gcc ctg gcg cat ggc gtc cgg gtt ctg gag gac	480
Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	
145 150 155 160	

ggc	gtg	aac	tat	gca	aca	ggg	aat	ctg	ccc	ggt	tgc	tct	ttc	tct	atc	528
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	
				165					170						175	
ttc	ctc	tta	gct	ttg	ctg	tct	tgt	ttg	acc	atc	cca	gct	tcc	gct	tac	576
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	
			180					185					190			
gag	gtg	cgc	aac	gtg	tcc	ggg	ata	tac	cat	gtc	acg	aac	gac	tgc	tcc	624
Glu	Val	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	
			195				200					205				
aac	tca	agt	att	gtg	tat	gag	gca	gcg	gac	atg	atc	atg	cac	acc	ccc	672
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	
	210						215				220					
ggg	tgc	gtg	ccc	tgc	gtc	cgg	gag	agt	aat	ttc	tcc	cgt	tgc	tgg	gta	720
Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Ser	Asn	Phe	Ser	Arg	Cys	Trp	Val	
225					230					235					240	
gcg	ctc	act	ccc	acg	ctc	gcg	gcc	agg	aac	agc	agc	atc	ccc	acc	acg	768
Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser	Ser	Ile	Pro	Thr	Thr	
				245					250					255		
aca	ata	cga	cgc	cac	gtc	gat	ttg	ctc	gtt	ggg	gcg	gct	gct	ctc	tgt	816
Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Leu	Cys	
			260					265					270			
tcc	gct	atg	tac	gtt	ggg	gat	ctc	tgc	gga	tcc	gtt	ttt	ctc	gtc	tcc	864
Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	
		275					280					285				
cag	ctg	ttc	acc	ttc	tca	cct	cgc	cgg	tat	gag	acg	gta	caa	gat	tgc	912
Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	Arg	Tyr	Glu	Thr	Val	Gln	Asp	Cys	
	290					295					300					
aat	tgc	tca	atc	tat	ccc	ggc	cac	gta	tca	ggt	cac	cgc	atg	gct	tgg	960
Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	
305					310					315					320	
gat	atg	atg	atg	aac	tgg	tca	cct	aca	acg	gcc	cta	gtg	gta	tcg	cag	1008
Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	
				325					330					335		
cta	ctc	cgg	atc	cca	caa	gcc	gtc	gtg	gac	atg	gtg	gcg	ggg	gcc	cac	1056
Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	
			340				345						350			
tgg	ggt	gtc	cta	gcg	ggc	ctt	gcc	tac	tat	tcc	atg	gtg	ggg	aac	tgg	1104
Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	
		355					360					365				
gct	aag	gtc	ttg	att	gtg	atg	cta	ctc	ttt	gct	ggc	gtt	gac	ggg	cac	1152
Ala	Lys	Val	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	
	370					375				380						
acc	cac	gtg	aca	ggg	gga	agg	gta	gcc	tcc	agc	acc	cag	agc	ctc	gtg	1200
Thr	His	Val	Thr	Gly	Gly	Arg	Val	Ala	Ser	Ser	Thr	Gln	Ser	Leu	Val	
385					390					395					400	

tcc tgg ctc tca caa ggg cca tct cag aaa atc caa ctc gtg aac acc Ser Trp Leu Ser Gln Gly Pro Ser Gln Lys Ile Gln Leu Val Asn Thr 405 410 415	1248
aac ggc agc tgg cac atc aac agg acc gct ctg aat tgc aat gac tcc Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser 420 425 430	1296
ctc caa act ggg ttc att gct gcg ctg ttc tac gca cac agg ttc aac Leu Gln Thr Gly Phe Ile Ala Ala Leu Phe Tyr Ala His Arg Phe Asn 435 440 445	1344
gcg tcc gga tgt cca gag cgc atg gcc agc tgc cgc ccc atc gac aag Ala Ser Gly Cys Pro Glu Arg Met Ala Ser Cys Arg Pro Ile Asp Lys 450 455 460	1392
ttc gct cag ggg tgg ggt ccc atc act cac gtt gtg cct aac atc tcg Phe Ala Gln Gly Trp Gly Pro Ile Thr His Val Val Pro Asn Ile Ser 465 470 475 480	1440
gac cag agg cct tat tgc tgg cac tat gca ccc caa ccg tgc ggt att Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Gln Pro Cys Gly Ile 485 490 495	1488
gta ccc gcg tcg cag gtg tgt ggc cca gtg tat tgc ttc acc ccg agt Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser 500 505 510	1536
cct gtt gtg gtg ggg acg acc gac cgt tcc gga gtc ccc acg tat agc Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Val Pro Thr Tyr Ser 515 520 525	1584
tgg ggg gag aat gag aca gac gtg ctg cta ctc aac aac acg cgg ccg Trp Gly Glu Asn Glu Thr Asp Val Leu Leu Asn Asn Thr Arg Pro 530 535 540	1632
ccg caa ggc aac tgg ttc ggc tgt aca tgg atg aat agc acc ggg ttc Pro Gln Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe 545 550 555 560	1680
acc aag acg tgc ggg ggc ccc ccg tgt aac atc ggg ggg gtt ggc aac Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Val Gly Asn 565 570 575	1728
aac acc ttg att tgc ccc acg gat tgc ttc cga aag cac ccc gag gcc Asn Thr Leu Ile Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala 580 585 590	1776
act tac acc aaa tgc ggc tcg ggt cct tgg ttg aca cct agg tgt cta Thr Tyr Thr Lys Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Leu 595 600 605	1824
gtt gac tac cca tac aga ctt tgg cac tac ccc tgc act atc aat ttt Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile Asn Phe 610 615 620	1872
acc atc ttc aag gtc agg atg tac gtg ggg ggc gtg gag cac agg ctc Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Leu 625 630 635 640	1920

aac gcc gcg tgc aat tgg acc cga gga gag cgc tgt gac ctg gag gac 1968
 Asn Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp
 645 650 655

agg gat aga tca gag ctt agc ccg ctg cta ttg tct aca acg gag tgg 2016
 Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp
 660 665 670

cag gta ctg ccc tgt tcc ttt acc acc cta ccg gct ctg tcc act gga 2064
 Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly
 675 680 685

ttg atc cac ctc cat cag aat atc gtg gac gtg caa tac ctg tac ggt 2112
 Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly
 690 695 700

gta ggg tca gtg gtt gtc tcc gtc gta atc aaa tgg gag tat gtt ctg 2160
 Val Gly Ser Val Val Val Ser Val Val Ile Lys Trp Glu Tyr Val Leu
 705 710 715 720

ctg ctc ttc ctt ctc ctg gcg gac gcg cgc gtc tgt gcc tgc ttg tgg 2208
 Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ala Cys Leu Trp
 725 730 735

atg atg ctg ctg ata gcc cag gct gag gcc tga 2241
 Met Met Leu Leu Ile Ala Gln Ala Glu Ala
 740 745

<210> 8

<211> 746

<212> PRT

<213> Artificial sequence

<220>

<223> sequence coding for CE1E2

<400> 8

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110

Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	
		115					120					125				
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	
	130					135					140					
Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	
145					150					155					160	
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	
				165					170					175		
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	
			180					185					190			
Glu	Val	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	
		195					200					205				
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	
	210					215					220					
Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Ser	Asn	Phe	Ser	Arg	Cys	Trp	Val	
225					230					235					240	
Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser	Ser	Ile	Pro	Thr	Thr	
				245					250					255		
Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Leu	Cys	
			260					265					270			
Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	
		275					280					285				
Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	Arg	Tyr	Glu	Thr	Val	Gln	Asp	Cys	
	290					295					300					
Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	
305					310					315					320	
Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	
				325					330					335		
Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	
			340					345					350			
Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	
		355					360					365				
Ala	Lys	Val	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	
	370					375					380					
Thr	His	Val	Thr	Gly	Gly	Arg	Val	Ala	Ser	Ser	Thr	Gln	Ser	Leu	Val	
385					390					395					400	
Ser	Trp	Leu	Ser	Gln	Gly	Pro	Ser	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr	
				405					410					415		
Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser	
			420					425					430			

Leu Gln Thr Gly Phe Ile Ala Ala Leu Phe Tyr Ala His Arg Phe Asn
 435 440 445
 Ala Ser Gly Cys Pro Glu Arg Met Ala Ser Cys Arg Pro Ile Asp Lys
 450 455 460
 Phe Ala Gln Gly Trp Gly Pro Ile Thr His Val Val Pro Asn Ile Ser
 465 470 475 480
 Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Gln Pro Cys Gly Ile
 485 490 495
 Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser
 500 505 510
 Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Val Pro Thr Tyr Ser
 515 520 525
 Trp Gly Glu Asn Glu Thr Asp Val Leu Leu Leu Asn Asn Thr Arg Pro
 530 535 540
 Pro Gln Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe
 545 550 555 560
 Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Val Gly Asn
 565 570 575
 Asn Thr Leu Ile Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala
 580 585 590
 Thr Tyr Thr Lys Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Leu
 595 600 605
 Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile Asn Phe
 610 615 620
 Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Leu
 625 630 635 640
 Asn Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp
 645 650 655
 Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp
 660 665 670
 Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly
 675 680 685
 Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly
 690 695 700
 Val Gly Ser Val Val Val Ser Val Val Ile Lys Trp Glu Tyr Val Leu
 705 710 715 720
 Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ala Cys Leu Trp
 725 730 735
 Met Met Leu Leu Ile Ala Gln Ala Glu Ala
 740 745

<210> 9
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer oIV166

<400> 9
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<210> 10
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
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<400> 10
 gggggggacgc gtttagcatg gcgtggagca gt 32

<210> 11
 <211> 30
 <212> DNA
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<220>
 <223> primer oIV232

<400> 11
 gggggggagat ctccagcagg cagaagtatg 30

<210> 12
 <211> 33
 <212> DNA
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<220>
 <223> primer oIV233

<400> 12
 ggggggggtcg accgaaaatg gatatacaag ctc 33

<210> 13
 <211> 35
 <212> DNA
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<220>
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<400> 13
 ggggggtcta gaatgtcaat gtcctacaca tggac 35

<210> 14
 <211> 32
 <212> DNA
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<220>
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<400> 14
 ggggggtcta gattaccggt tggggagcag gt

32

<210> 15
 <211> 32
 <212> DNA
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<220>
 <223> primer oIV225

<400> 15
 ggggggctgc agatggcgcc tatcacggcc ta

32

<210> 16
 <211> 32
 <212> DNA
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<220>
 <223> primer oIV226

<400> 16
 ggggggtcta gattagcatg gcgtggagca gt

32

<210> 17
 <211> 35
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<220>
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<400> 17
 gggggggtcg acatgtcaat gtcctacaca tggac

35

<210> 18
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<220>
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<400> 18
 gggggggcat gcttaccggt tggggagcag gt

32

<210> 19
 <211> 33
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<220>
 <223> primer oIV229

<400> 19
 ggggggtcta gaccggtagt tcgcatatac ata

33

<210> 20
 <211> 33
 <212> DNA
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<220>
 <223> primer oIV172

<400> 20
 ggggggggta ccatgtccgg ctcgtggcta agg

33

<210> 21
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<220>
 <223> primer oIV173

<400> 21
 ggggggtcta gattagcagc agacgatgtc gtc

33

<210> 22
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<220>
 <223> primer oIV62

<400> 22
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33

<210> 23
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<220>
 <223> primer oIV68

<400> 23
 ggggggtcta gatcaggcct cagcctgggc tat

33

<210> 24
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 <212> PRT
 <213> Artificial sequence

<220>
 <223> epitope GLL

<400> 24

Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu
 1 5 10

<210> 25
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> epitope ALY

<400> 25

Ala Leu Tyr Asp Val Val Ser Thr Leu
 1 5

<210> 26
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> epitope KLQ

<400> 26

Lys Leu Gln Asp Cys Thr Met Leu Val
 1 5

<210> 27
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> epitope DLM

<400> 27

Asp Leu Met Gly Tyr Ile Pro Leu Val
 1 5